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**ABSTRACT:** The optimal contribution selection method and the simulated annealing algorithm were used to maximize the genetic gain and reduce inbreeding in fish breeding populations. This study considered the following mating designs: full factorial (3 x 3); full factorial (6 x 6) and nested (6 males x 18 females). A quantitative trait based on a strictly additive and polygenic model was simulated. Two levels for the number of genotyped offspring (360 or 720) and three levels of heritability (0.1; 0.3; 0.5) were assumed. The best results in terms of ΔF and ΔG were obtained with the full factorial design (6 x 6) and considering a trait with a high heritability. The optimal family size was found at 20 fish per mating.

**Key words:** Simulation, Fish, optimum contribution, Annealing algorithm.

**INTRODUCTION** – The design of optimal mating schemes is a mean to improve fish performance worldwide. During the last two decades, breeding strategies and techniques addressing both genetic improvement has been well documented and applied in several countries (Sonesson *et al*., 2005). Nevertheless, in Italy, selective breeding has not been widely practiced in fish farming. Recent advances in fish breeding involve comparisons and optimization of mating designs using advanced analytical models as the optimum contribution selection (Meuwissen, 1997) and the simulated annealing algorithm (Press *et al*., 1989). The high reproductive potential in fish species allows high genetic gains by applying high selection intensities. This means that a very small number of individuals are used to generate successive generations and hence the rate of inbreeding can be high (Sonesson *et al*., 2005). The detrimental effects of inbreeding are well documented in fish. In recent years, many selection and mating strategies have been proposed to restrict inbreeding in selection programmes (Sonesson *et al*., 2005). In this study, a stochastic simulation was used to optimize mating schemes using different genetic parameters and under restricted inbreeding in fish breeding.

**MATERIAL AND METHODS** – A fish population under artificial selection was modelled by stochastic (Monte Carlo) simulation using Mathlab software. Selection was applied for a single trait measured on both sexes and based on estimated breeding values (EBVs) using the ASREML2 statistical package. Generation were discrete (equal number of sires and dams were selected at each generation). The trait under selection was assumed to be determined by an infinite number of unlinked additive loci, each with an infinitesimal effect. The trait was considered to be standardized, so the initial phenotypic variance is unity. Phenotypes of unrelated base population animals (generation 0) were generated as the sum of a normally distributed environmental and genetic effects. Phenotipic values of the offspring born every generation were generated as: $P = \mu + (\sigma_A\ RND(0,1)_S + \sigma_A\ RND(0,1)_D)/2 + \sigma_E\ RND(0,1) + (0.5(1-(F_s+F_d)/2))^{1/2}\ \sigma_A\ ^{*}RND(0,1)$ where $\sigma_{A\,(1)} = \sigma_{A\,(0)}/(1+kh^2_{(1)})$ and $k=(0.5)(k_m+k_f)$; $k_y = i_y(i_y-x_y)$ y=male or female. Selection was directional upwards and by truncation. Total number of offspring born per generation and numbers of selected males and females were constant (10 or 20 offspring per mating) over generations and varied according to the mating schemes. The simulated breeding schemes are described in Table 1.

Table 1. Parameters of the closed nucleus scheme.

| | |
|---|---|
| Number of selection candidates per generation | 0 or 180 or 360 or 720 |
| Number of generations | 10 |
| Number of replicated simulations | 100 |
| Mating schemes | factorial 3 x 3; 6 x 6; nested 6 (males) x 18 (females) |
| Heritability | 0.1 or 0.3 or 0.5 |

The method of Meuwissen (1997) was used to select animals. This method maximises the genetic level of the next generation of animals $G_{t+1} = c'EBV_t$ where $c_t$ is a vector of genetic contributions of selected candidates to generation $t_{+1}$ and EBVs is a vector of best linear unbiased prediction (BLUP) estimates of candidates in generation t. Rates of inbreeding are controlled by constraining the average coancestry to $C_{t+1} = c A_t c_t/2$ where $A_t$ is a (n x n) relationship matrix among n selection candidates $Ct_{+1} = 1-(1-\Delta Ft)^t$ and $\Delta F_d$ is the desidered rate of inbreeding. For optimizing of $c_t$, it was also necessary to constrain the sum the contributions of males (females) to $^1/_2$. In order to obtain the optimal $c_t$ that maximize $G_{t+1}$ Lagrangian multipliers were used. An additional restriction was to select only one full sibs per family. The minimum coancestry mating (reduce the average relationship of sires and dams and therefore also the inbreeding of their progeny is minimized) was obtained by applying the simulated annealing algorithm according to Press *et al*. (1989)

**RESULTS AND CONCLUSIONS** – The rate of inbreeding (ΔF) and genetic gain (ΔG) for the three mating designs are reported in Table 2.

Table 2. Rate of inbreeding (ΔF)(x100) and genetic gain (DG))(σp) for different mating schemes and genetic parameters.

| | N. of offsprings per family | | | | | |
|---|---|---|---|---|---|---|
| | 10 | | | 20 | | |
| Heritability | 0.1 | 0.3 | 0.5 | 0.1 | 0.3 | 0.5 |
| Full factorial (3 x 3) | | | | | | |
| ΔF | 3.96 | 5.00 | 4.55 | 4.50 | 4.70 | 4.65 |
| ΔG | 0.29 | 0.60 | 0.75 | 0.37 | 0.60 | 0.97 |
| Full factorial (6 x 6) | | | | | | |
| ΔF | 2.25 | 2.20 | 2.10 | 2.05 | 1.80 | 1.85 |
| ΔG | 0.38 | 0.64 | 0.76 | 0.47 | 0.69 | 0.94 |
| Nested (6males x 18 females) | | | | | | |
| ΔF | 2.60 | 2.25 | 2.36 | 2.06 | 2.90 | 2.05 |
| ΔG | 0.43 | 0.72 | 0.86 | 0.57 | 0.66 | 0.89 |

The full factorial design gives the best results in terms of ΔF and ΔG (1.85 and 0.94 or 1.80 and 0.69) for a maximal number of sires and dams (6 x 6), higher size of families per mating used for selection (720 offspings) and higher heritability (0.3 or 0.5). According to Sorensen *et al*. (2005) the superiority of the factorial mating compared to hierarchical scheme can be explained in terms of the different genetic structure of populations obtained showing, in the factorial design, small full-sibs families, more paternal half-sibs and a group of maternal half-sibs. At a lower heritability (0.1) the nested design become competitive with the full factorial mating (6 x 6). In conclusion, the optimal design to estimate additive effects in fish seems to be a full factorial mating with full-sibs families of 20 animals.

**REFERENCES** – **Meuwissen**, T.H.E., 1997. Maximizing the response of selection. with a predefined rate of inbreeding. J. Anim.Sci. 75:924-940. **Press**, W.H., Flannery B.P., Teukolsky, S.A., Vetterling, W.T., 1989. Minimization or maximization of function. In: Numerical recipes. The act of scientific computing. University of Cambridge Press, pp. 274-334. **Sonesson**, A.K., Gjerde, B., Meuwissen, T.H.E., 2005. Truncation selection of BLUP-EBV and phenotypic values in fish breeding schemes. Aquaculture 243:61-68. **Sorensen**, A.C., Berg, P., Woolliams, J.A., 2005. The advantage of factorial mating under selection is uncovered by deterministically predicted rates of inbreeding. Genet. Sel. Evol. 37:57-81.